# RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: _09/806,232_

Source: _PCTO9_

Date Processed by STIC: _4-4-01_

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2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
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Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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PCT
09

RAW SEQUENCE LISTING   DATE: 04/04/2001
PATENT APPLICATION: US/09/806,232   TIME: 11:23:01

        Input Set : A:\1241.18 Seq List.txt
        Output Set: N:\CRF3\04042001\I806232.raw

          3 <110> APPLICANT: Seiki Motoharu
          5 <120> TITLE OF INVENTION: DNA CODING FOR NOVEL POLIPEPTIDE
W-->   7 <130> FILE REFERENCE:
C-->   9 <140> CURRENT APPLICATION NUMBER: US/09/806,232
C-->   10 <141> CURRENT FILING DATE: 2001-03-28
         12 <150> PRIOR APPLICATION NUMBER: JP10-276258
         13 <151> PRIOR FILING DATE: 1998-09-29
         15 <150> PRIOR APPLICATION NUMBER: JP10-291505
         16 <151> PRIOR FILING DATE: 1998-09-29
         18 <160> NUMBER OF SEQ ID NOS: 22
         20 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
Corrected Diskette Needed
See pp. 1-8

ERRORED SEQUENCES

        259 <210> SEQ ID NO: 3
        260 <211> LENGTH: 3517
E-->   261 <212> TYPE:
        262 <213> ORGANISM: Mouse

Missing mandatory sequence type
DNA, RNA, PRT

        264 <220> FEATURE:
        265 <221> NAME/KEY: CDS
        266 <222> LOCATION: (86)..(1846)
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        272   Met Gly Arg Arg Pro Arg Gly Pro Gly
        273   1   5
        275 tcc ccc cgg gga cct ggc cct cca cgc ccc ggg ccg ggg ctg cca cca 160
        276 Ser Pro Arg Gly Pro Gly Pro Pro Arg Pro Gly Pro Gly Leu Pro Pro
        277 10   15   20   25
        279 ctg ctg ctt gta ctg gcg ctg gcg gcc cat ggg ggc tgc gca gcg ccc 208
        280 Leu Leu Leu Val Leu Ala Leu Ala Ala His Gly Gly Cys Ala Ala Pro
        281   30   35   40
        283 gcg ccc cgc gcg gag gac ctc agc ctc ggg gtg gag tgg cta agc agg 256
        284 Ala Pro Arg Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg
        285   45   50   55
        287 ttt ggc tac ctg ccg cct gca gat ccg gca tca ggg cag cta cag acc 304
        288 Phe Gly Tyr Leu Pro Pro Ala Asp Pro Ala Ser Gly Gln Leu Gln Thr
        289   60   65   70
        291 cag gag gaa ctg tcc aaa gcg att act gcc atg cag cag ttt ggt ggt 352
        292 Gln Glu Glu Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly
        293   75   80   85
        295 ctg gag acc act ggc atc cta gat gag gcc act ctg gcc ctg atg aaa 400
        296 Leu Glu Thr Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys
        297 90   95   100   105
        299 acc cct cga tgc tcc ctt ccg gac ctg ccc cct ggg gcc caa tcg aga 448
        300 Thr Pro Arg Cys Ser Leu Pro Asp Leu Pro Pro Gly Ala Gln Ser Arg

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001
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Input Set : A:\1241.18 Seq List.txt
Output Set: N:\CRF3\04042001\I806232.raw

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303 agg aag cgg cag act cca ccc cca acc aaa tgg agc aag agg aac ctt   496
304 Arg Lys Arg Gln Thr Pro Pro Pro Thr Lys Trp Ser Lys Arg Asn Leu
305                 125               130               135
307 tct tgg agg gtc cgg aca ttc cca cgg gac tca ccc ctg ggc cgg gat   544
308 Ser Trp Arg Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly Arg Asp
309                 140               145               150
311 act gtg cgt gca ctc atg tac tac gcc ctc aaa gtc tgg agt gac atc   592
312 Thr Val Arg Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile
313                 155               160               165
315 aca ccc ttg aac ttc cac gag gta gcg ggc aac gcg gcg gac atc cag   640
316 Thr Pro Leu Asn Phe His Glu Val Ala Gly Asn Ala Ala Asp Ile Gln
317 170                 175               180               185
319 atc gac ttc tcc aag gcc gac cac aat gac ggc tac ccc ttc gat ggc   688
320 Ile Asp Phe Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly
321                 190               195               200
323 cct ggt ggc acg gtg gcc cac gca ttc ttc cct ggt gac cac cac acg   736
324 Pro Gly Gly Thr Val Ala His Ala Phe Phe Pro Gly Asp His His Thr
325                 205               210               215
327 gca ggg gac acc cac ttt gat gac gat gag cca tgg acc ttc cgt tcc   784
328 Ala Gly Asp Thr His Phe Asp Asp Asp Glu Pro Trp Thr Phe Arg Ser
329                 220               225               230
331 tca gat gcc cac ggg atg gac ctg ttt gca gtg gcc gtc cat gag ttt   832
332 Ser Asp Ala His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe
333     235                 240               245
335 ggt cat gcc att ggt ctg agc cat gtt gcc gcc cca agc tcc atc atg   880
336 Gly His Ala Ile Gly Leu Ser His Val Ala Ala Pro Ser Ser Ile Met
337 250                 255               260               265
339 caa ccg tac tac cag ggc ccc gtg ggt gac ccc gta cgc tat gga ctt   928
340 Gln Pro Tyr Tyr Gln Gly Pro Val Gly Asp Pro Val Arg Tyr Gly Leu
341                 270               275               280
343 ccc tat gag gac agg gtg cgt gtc tgg cag ttg tac ggt gtg cgg gaa   976
344 Pro Tyr Glu Asp Arg Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu
345                 285               290               295
347 tcc gtg tcc cct act gcc cag ctg gat acc cca gag ccc gag gag cca   1024
348 Ser Val Ser Pro Thr Ala Gln Leu Asp Thr Pro Glu Pro Glu Glu Pro
349                 300               305               310
351 ccc ctc ctg cca gag ccc ccc aac aat cgg tct agc act ccg ccc cag   1072
352 Pro Leu Leu Pro Glu Pro Pro Asn Asn Arg Ser Ser Thr Pro Pro Gln
353     315                 320               325
355 aag gac gtg cct cac agg tgc act gcc cac ttt gat gct gtg gcc cag   1120
356 Lys Asp Val Pro His Arg Cys Thr Ala His Phe Asp Ala Val Ala Gln
357 330                 335               340               345
359 att cga ggc gaa gca ttc ttt ttc aaa ggc aag tat ttc tgg agg ctg   1168
360 Ile Arg Gly Glu Ala Phe Phe Phe Lys Gly Lys Tyr Phe Trp Arg Leu
361                 350               355               360
363 acc cgg gac cga cac ttg gtg tcg ctg cag ccg gct caa atg cat cgc   1216
364 Thr Arg Asp Arg His Leu Val Ser Leu Gln Pro Ala Gln Met His Arg
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367 ttc tgg cgg ggc ctg ccg ctg cac ctg gac agt gtg gac gcc gtg tat   1264
368 Phe Trp Arg Gly Leu Pro Leu His Leu Asp Ser Val Asp Ala Val Tyr
369         380                 385                 390
371 gag cgt acc agt gac cac aag att gtc ttc ttc aaa gga gac aga tac   1312
372 Glu Arg Thr Ser Asp His Lys Ile Val Phe Phe Lys Gly Asp Arg Tyr
373         395                 400                 405
375 tgg gtg ttt aag gac aac aac gta gag gaa ggg tac ccg cga cct gtc   1360
376 Trp Val Phe Lys Asp Asn Asn Val Glu Glu Gly Tyr Pro Arg Pro Val
377 410                 415                 420                 425
379 tcc gac ttc agc ctc ccg cca ggt ggc atc gat gct gtc ttc tcc tgg   1408
380 Ser Asp Phe Ser Leu Pro Pro Gly Gly Ile Asp Ala Val Phe Ser Trp
381         430                 435                 440
383 gcc cac aat gac agg act tat ttc ttt aag gac cag ctg tac tgg cgc   1456
384 Ala His Asn Asp Arg Thr Tyr Phe Phe Lys Asp Gln Leu Tyr Trp Arg
385         445                 450                 455
387 tat gat gac cac aca cgg cgc atg gac cct ggc tac cct gcc cag gga   1504
388 Tyr Asp Asp His Thr Arg Arg Met Asp Pro Gly Tyr Pro Ala Gln Gly
389         460                 465                 470
391 ccc ctg tgg aga ggt gtc ccc agc atg ttg gat gat gcc atg cgc tgg   1552
392 Pro Leu Trp Arg Gly Val Pro Ser Met Leu Asp Asp Ala Met Arg Trp
393         475                 480                 485
395 tct gat ggt gca tcc tat ttc ttc cga ggc cag gag tac tgg aaa gtg   1600
396 Ser Asp Gly Ala Ser Tyr Phe Phe Arg Gly Gln Glu Tyr Trp Lys Val
397 490                 495                 500                 505
399 ctg gat ggc gag ctg gaa gca gcc ccc ggg tac cca cag tct aca gcc   1648
400 Leu Asp Gly Glu Leu Glu Ala Ala Pro Gly Tyr Pro Gln Ser Thr Ala
401                 510                 515                 520
403 cgc gac tgg ctg gta tgc ggt gag ccg ctg gcg gat gcg gag gat gta   1696
404 Arg Asp Trp Leu Val Cys Gly Glu Pro Leu Ala Asp Ala Glu Asp Val
405                 525                 530                 535
407 ggg cct gga ccc cag ggc cgc agt ggg gcc caa gat ggt ctg gca gta   1744
408 Gly Pro Gly Pro Gln Gly Arg Ser Gly Ala Gln Asp Gly Leu Ala Val
409         540                 545                 550
411 tgt tcc tgc act tca gac gca cac agg ttg gca ctg cca tct ctg ctg   1792
412 Cys Ser Cys Thr Ser Asp Ala His Arg Leu Ala Leu Pro Ser Leu Leu
413         555                 560                 565
415 ctt ctg act cca ctg ctg tgg ggc ctg tgg acc tca gtc tct gcc aag   1840
416 Leu Leu Thr Pro Leu Leu Trp Gly Leu Trp Thr Ser Val Ser Ala Lys
417 570               .    575                 580                 585
419 gca tcc tgagggcagt gctagccttg cggatcaagg agccagggga gcagggacac   1896
420 Ala Ser
422 actggccagt actcagcagg acttgtgctc caagcttccg gtccctcgct ccttccttcc   1956
424 ttccttcctt gaacccaggg gtgctgtgcc atctgctgga gtggtctcca gctgggacag   2016
426 gacgtcccac caagggcatc catgcacacc ttgcctacct ggagcagcca taggcagctc   2076
428 cccttccctc ctctgcacat cacgctgctt cgttgcacct tgccgggctg cccaagccca   2136
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434 tcacaagtaa gagagttgat gccccgatgg gggaacaggg tgggagaaag gcacctaccc   2316
436 agaagtctga tccactgccg tttgcagcag ccagcgccgt atctgctggg ataggggacc   2376
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446 gcccccatat agttctggcc tgagaccctg cagcttggac tcacagctgt cccctcccca 2676
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456 taatgagctc cagaaaggaa cagccaagtt caaaggttct gggacaagac gggcctgagg 2976
458 aacagggcca cccaggtagg cgtggctgta gggtaagcag tttctgtcat tgggcacgag 3036
460 atgaaaatta gtgatcacac gcacataccc ccctccccaa ctggcccggt cccatctcag 3096
462 gtaagaaagg cttctgtcta ccccaggcca ggtttgagtg ttgtcaggat gagtgagcag 3156
464 ctagcggggc ctaagtttct accctccatt tcccaagcct ggccacaccc tagacccctg 3216
466 tcagactagg caggacagag tcaggggtag gggcatctga ggtttccctg tcttggaagc 3276
468 caccctactc tgccctcata tcaaagcacg ctcctatgat gtcccatgtt gtccaccagc 3336
470 ctgcaggaca cagatgtcct atacagcaac agggaaagtc caaaaatctt tgtcacatag 3396
472 cactgaaaac cagacccgca ggctggagct gtctagatgc tggtgtcaca ctcattttaa 3456
474 aacccaaact cttaataaaa attttgtaca ctggaaaaaa aaaaaaaaa aaaaaaaaa 3516
476 a                                                                3517
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481 <213> ORGANISM: Homo sapiens
483 <220> FEATURE:
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485 <222> LOCATION: (100)..(1917)
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491                                            Met Arg Arg Arg Ala
492                                            1
493             5
495 gcc cgg gga ccc ggc ccg ccg ccc cca ggg ccc gga ctc tcg cgg ctg  162
496 Ala Arg Gly Pro Gly Pro Pro Pro Gly Pro Gly Leu Ser Arg Leu
497             10              15              20
499 ccg ctg ctg ccg ctg ccg ctg ctg ctg ctg ctg gcg ctg ggg acc cgc  210
500 Pro Leu Leu Pro Leu Pro Leu Leu Leu Leu Leu Ala Leu Gly Thr Arg
501             25              30              35
503 ggg ggc tgc gcc gcg ccg gaa ccc gcg cgg cgc gcc gag gac ctc agc  258
504 Gly Gly Cys Ala Ala Pro Glu Pro Ala Arg Arg Ala Glu Asp Leu Ser
505         40              45              50
507 ctg gga gtg gag tgg cta agc agg ttc ggt tac ctg ccc ccg gct gac  306
508 Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr Leu Pro Pro Ala Asp
509     55              60              65
511 ccc aca aca ggg cag ctg cag acg caa gag gag ctg tct aag gcc atc  354
512 Pro Thr Thr Gly Gln Leu Gln Thr Gln Glu Glu Leu Ser Lys Ala Ile
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E--> 480 <212> TYPE: ⟶ *Missing mandatory sequence type*

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520 Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg Cys Ser Leu Pro Asp
521             105                 110                115
523 ctc cct gtc ctg acc cag gct cgc agg aga cgc cag gct cca gcc ccc    498
524 Leu Pro Val Leu Thr Gln Ala Arg Arg Arg Arg Gln Ala Pro Ala Pro
525             120                 125                130
527 acc aag tgg aac aag agg aac ctg tcg tgg agg gtc cgg acg ttc cca    546
528 Thr Lys Trp Asn Lys Arg Asn Leu Ser Trp Arg Val Arg Thr Phe Pro
529             135                 140                145
531 cgg gac tca cca ctg ggg cac gac acg gtg cgt gca ctc atg tac tac    594
532 Arg Asp Ser Pro Leu Gly His Asp Thr Val Arg Ala Leu Met Tyr Tyr
533 150             155                 160                165
535 gcc ctc aag gtc tgg agc gac att gcg ccc ctg aac ttc cac gag gtg    642
536 Ala Leu Lys Val Trp Ser Asp Ile Ala Pro Leu Asn Phe His Glu Val
537             170                 175                180
539 gcg ggc agc acc gcc gac atc cag atc gac ttc tcc aag gcc gac cat    690
540 Ala Gly Ser Thr Ala Asp Ile Gln Ile Asp Phe Ser Lys Ala Asp His
541             185                 190                195
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544 Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly Thr Val Ala His Ala
545             200                 205                210
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548 Phe Phe Pro Gly His His His Thr Ala Gly Asp Thr His Phe Asp Asp
549     215                 220                 225
551 gac gag gcc tgg acc ttc cgc tcc tcg gat gcc cac ggg atg gac ctg    834
552 Asp Glu Ala Trp Thr Phe Arg Ser Ser Asp Ala His Gly Met Asp Leu
553 230             235                 240                245
555 ttt gca gtg gct gtc cac gag ttt ggc cac gcc att ggg tta agc cat    882
556 Phe Ala Val Ala Val His Glu Phe Gly His Ala Ile Gly Leu Ser His
557             250                 255                260
559 gtg gcc gct gca cac tcc atc atg cgg ccg tac tac cag ggc ccg gtg    930
560 Val Ala Ala Ala His Ser Ile Met Arg Pro Tyr Tyr Gln Gly Pro Val
561             265                 270                275
563 ggt gac ccg ctg cgc tac ggg ctc ccc tac gag gac aag gtg cgc gtc    978
564 Gly Asp Pro Leu Arg Tyr Gly Leu Pro Tyr Glu Asp Lys Val Arg Val
565             280                 285                290
567 tgg cag ctg tac ggt gtg cgg gag tct gtg tct ccc acg gcg cag ccc    1026
568 Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser Pro Thr Ala Gln Pro
569     295                 300                 305
571 gag gag cct ccc ctg ctg ccg gag ccc cca gac aac cgg tcc agc gcc    1074
572 Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro Asp Asn Arg Ser Ser Ala
573 310             315                 320                325
575 ccg ccc agg aag gac gtg ccc cac aga tgc agc act cac ttt gac gcg    1122
576 Pro Pro Arg Lys Asp Val Pro His Arg Cys Ser Thr His Phe Asp Ala
577             330                 335                340
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580 Val Ala Gln Ile Arg Gly Glu Ala Phe Phe Phe Lys Gly Lys Tyr Phe
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585         360              365              370
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588 Met His Arg Phe Trp Arg Gly Leu Pro Leu His Leu Asp Ser Val Asp
589     375              380              385
591 gcc gtg tac gag cgc acc agc gac cac aag atc gtc ttc ttt aaa gga   1314
592 Ala Val Tyr Glu Arg Thr Ser Asp His Lys Ile Val Phe Phe Lys Gly
593 390              395              400              405
595 gac agg tac tgg gtg ttc aag gac aat aac gta gag gaa gga tac ccg   1362
596 Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn Val Glu Glu Gly Tyr Pro
597              410              415              420
599 cgc ccc gtc tcc gac ttc agc ctc ccg cct ggc ggc atc gac gct gcc   1410
600 Arg Pro Val Ser Asp Phe Ser Leu Pro Pro Gly Gly Ile Asp Ala Ala
601              425              430              435
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604 Phe Ser Trp Ala His Asn Asp Arg Thr Tyr Phe Phe Lys Asp Gln Leu
605         440              445              450
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608 Tyr Trp Arg Tyr Asp Asp His Thr Arg His Met Asp Pro Gly Tyr Pro
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612 Ala Gln Ser Pro Leu Trp Arg Gly Val Pro Ser Thr Leu Asp Asp Ala
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615 atg cgc tgg tcc gac ggt gcc tcc tac ttc ttc cgt ggc cag gag tac   1602
616 Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe Phe Arg Gly Gln Glu Tyr
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619 tgg aaa gtg ctg gat ggc gag ctg gag gtg gca ccc ggg tac cca cag   1650
620 Trp Lys Val Leu Asp Gly Glu Leu Glu Val Ala Pro Gly Tyr Pro Gln
621         505              510              515
623 tcc acg gcc cgg gac tgg ctg gtg tgt gga gac tca cag gcc gat gga   1698
624 Ser Thr Ala Arg Asp Trp Leu Val Cys Gly Asp Ser Gln Ala Asp Gly
625         520              525              530
627 tct gtg gct gcg ggc gtg gac gcg gca gag ggg ccc cgc gcc cct cca   1746
628 Ser Val Ala Ala Gly Val Asp Ala Ala Glu Gly Pro Arg Ala Pro Pro
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632 Gly Gln His Asp Gln Ser Arg Ser Glu Asp Gly Tyr Glu Val Cys Ser
633 550              555              560              565
635 tgc acc tct ggg gca tcc tct ccc ccg ggg gcc cca ggc cca ctg gtg   1842
636 Cys Thr Ser Gly Ala Ser Ser Pro Pro Gly Ala Pro Gly Pro Leu Val
637              570              575              580
639 gct gcc acc atg ctg ctg ctg ctg ccg cca ctg tca cca ggc gcc ctg   1890
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644 Trp Thr Ala Ala Gln Ala Leu Thr Leu
645         600              605
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RAW SEQUENCE LISTING   DATE: 04/04/2001
PATENT APPLICATION: US/09/806,232   TIME: 11:23:02

Input Set : A:\1241.18 Seq List.txt
Output Set: N:\CRF3\04042001\I806232.raw

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1384 <210> SEQ ID NO: 12
1385 <211> LENGTH: 22
E--> 1386 <212> TYPE:
1387 <213> ORGANISM: Homo sapiens
1389 <400> SEQUENCE: 12
1390 ggagctgtct aaggccatca ca                          22
1392 <210> SEQ ID NO: 13
1393 <211> LENGTH: 23
E--> 1394 <212> TYPE:
1395 <213> ORGANISM: Homo sapiens
1397 <400> SEQUENCE: 13
1398 ctccctacaa cccgaattcc tac                         23
1400 <210> SEQ ID NO: 14
1401 <211> LENGTH: 20
E--> 1402 <212> TYPE:
1403 <213> ORGANISM: Homo sapiens
1405 <400> SEQUENCE: 14
1406 cttgtgggca gataggggggc                            20
1408 <210> SEQ ID NO: 15
1409 <211> LENGTH: 21
E--> 1410 <212> TYPE:
1411 <213> ORGANISM: Homo sapiens
```
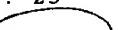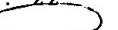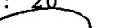
All missing mandatory sequence type.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001
TIME: 11:23:02

Input Set : A:\1241.18 Seq List.txt
Output Set: N:\CRF3\04042001\I806232.raw

```
      1413  <400> SEQUENCE: 15
      1414  cgcgccgagg acctcagcct g                                    21
      1416  <210> SEQ ID NO: 16
      1417  <211> LENGTH: 21
E-->  1418  <212> TYPE:
      1419  <213> ORGANISM: Homo sapiens
      1421  <400> SEQUENCE: 16
      1422  ggttcctctt gttccacttg g                                    21
      1656  <210> SEQ ID NO: 19
      1657  <211> LENGTH: 21
E-->  1658  <212> TYPE:
      1659  <213> ORGANISM: Homo sapiens
      1661  <400> SEQUENCE: 19
      1662  aatctcccat cggccctttc a                                    21
      1664  <210> SEQ ID NO: 20
      1665  <211> LENGTH: 20
E-->  1666  <212> TYPE:
      1667  <213> ORGANISM: Homo sapiens
      1669  <400> SEQUENCE: 20
      1670  atgcacggcc accaggaaga                                      20
      1672  <210> SEQ ID NO: 21
      1673  <211> LENGTH: 20
E-->  1674  <212> TYPE:
      1675  <213> ORGANISM: Homo sapiens
      1677  <400> SEQUENCE: 21
      1678  ggatcagaca acgatcgagt                                      20
      1680  <210> SEQ ID NO: 22
      1681  <211> LENGTH: 20
E-->  1682  <212> TYPE:
      1683  <213> ORGANISM: Homo sapiens
      1685  <400> SEQUENCE: 22
      1686  cagcttgaag ttgtgcgtct                                      20
```

All missing mandatory sequence type.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/806,232

DATE: 04/04/2001
TIME: 11:23:03

Input Set : A:\1241.18 Seq List.txt
Output Set: N:\CRF3\04042001\I806232.raw

L:7 M:201 W: Mandatory field data missing, FILE REFERENCE
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:261 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:480 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1362 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1370 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1378 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1386 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1394 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1402 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1410 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1418 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1658 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1666 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1674 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1682 M:310 E: (3) Wrong or Missing Sequence Type, TYPE: